

0570
0320
#5

Serial Number: 09/988,863A

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: **ENTERED**
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIIPE

RAW SEQUENCE LISTING

DATE: 03/25/2002

PATENT APPLICATION: US/09/988,863A

TIME: 09:53:09

Input Set : A:\pto_ms.txt

Output Set: N:\CRF3\03252002\I988863A.raw

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3 <110> APPLICANT: Bayer AG
5 <120> TITLE OF INVENTION: Plant phosphomevalonate kinases
7 <130> FILE REFERENCE: Le A 35 018
9 <140> CURRENT APPLICATION NUMBER: US/09/988,863A
10 <141> CURRENT FILING DATE: 2001-11-21
12 <160> NUMBER OF SEQ ID NOS: 5
14 <170> SOFTWARE: PatentIn Ver. 2.1
16 <210> SEQ ID NO: 1
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18 <212> TYPE: DNA
19 <213> ORGANISM: Arabidopsis thaliana
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30 tcagagggtgc cgaaccgaac cgaccgtaa accgaaatcc tcaaaagaaa ttgccgatcg 180
32 gtttgctact gttcaaaaacc tcggtgccga gaaccgaaac tgctcggtttt ttcggttcgg 240
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36 ttctcttttc atcggcgacg acgacgtcga gtttctgtca aaacgttaac gatccgactc 360
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40 cgatccgtct cgatcgacgg agaatacgtt tcgatccggt ttcgatccaa atcggagagt 480
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46 tccgatcatt tccggcgata tccaatcgca gactgaggtg aatctggggg tttgatcagc 660
48 gattatcttt gtcactcttt gaaa atg gct gtt gtt gct tct gct cct ggg 711
49 Met Ala Val Val Ala Ser Ala Pro Gly
50 1 5
52 aaa gtt ttg atg act gga ggc tac ctt gta ctc gag aag cca aat gca 759
53 Lys Val Leu Met Thr Gly Gly Tyr Leu Val Leu Glu Lys Pro Asn Ala
54 10 15 20 25
56 ggg ctt gtg ttg agt aca aat gca cgg ttt tac gcg att gtg aag cca 807
57 Gly Leu Val Leu Ser Thr Asn Ala Arg Phe Tyr Ala Ile Val Lys Pro
58 30 35 40
60 atc aac gaa gaa gtc aag cct gaa agt tgg gca tgg aaa tgg aca gat 855
61 Ile Asn Glu Glu Val Lys Pro Glu Ser Trp Ala Trp Lys Trp Thr Asp
62 45 50 55
64 gtc aaa tta aca tca cca cag ctc tcg aga gaa agc atg tat aaa ctg 903
65 Val Lys Leu Thr Ser Pro Gln Leu Ser Arg Glu Ser Met Tyr Lys Leu
66 60 65 70
68 tca ctg aat cat ttg act ctt cag tct gtg tct gca agt gat tca aga 951
69 Ser Leu Asn His Leu Thr Leu Gln Ser Val Ser Ala Ser Asp Ser Arg

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76	ttg gca acc gag aag gac aaa gaa tca ttg cac aaa ctc tta ttg caa	1047		
77	Leu Ala Thr Glu Lys Asp Lys Glu Ser Leu His Lys Leu Leu Leu Gln			
78		110	115	120
80	ggt ctt gat ata aca ata tta ggc tcc aat gac ttt tac tca tat cgg	1095		
81	Gly Leu Asp Ile Thr Ile Leu Gly Ser Asn Asp Phe Tyr Ser Tyr Arg			
82		125	130	135
84	aac cag ata gaa tcg gct ggg ctt cca ttg aca cca gaa tcg ctg ggt	1143		
85	Asn Gln Ile Glu Ser Ala Gly Leu Pro Leu Thr Pro Glu Ser Leu Gly			
86		140	145	150
88	acc ctt gca ccg ttt gca tca atc aca ttc aat gct gcg gag tca aat	1191		
89	Thr Leu Ala Pro Phe Ala Ser Ile Thr Phe Asn Ala Ala Glu Ser Asn			
90		155	160	165
92	ggt gct aat tcc aag cct gaa gta gca aaa act ggc tta ggt tct tct	1239		
93	Gly Ala Asn Ser Lys Pro Glu Val Ala Lys Thr Gly Leu Gly Ser Ser			
94	170	175	180	185
96	gca gca atg aca aca gct gtg gtt gca gct ctg tta cat tat ctt gga	1287		
97	Ala Ala Met Thr Thr Ala Val Val Ala Ala Leu Leu His Tyr Leu Gly			
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104	gat cta gat gtt atc cat atg ata gca caa acg tct cat tgt ctt gca	1383		
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108	caa ggg aag gtc gga agt ggg ttt gat gtc agc tgt gct gtc tat gga	1431		
109	Gln Gly Lys Val Gly Ser Gly Phe Asp Val Ser Cys Ala Val Tyr Gly			
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112	agt cag cgt tat gtt cgc ttc tct cca gaa gtc ttg tca ttt gct cag	1479		
113	Ser Gln Arg Tyr Val Arg Phe Ser Pro Glu Val Leu Ser Phe Ala Gln			
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116	gtt gca gta aca ggt ctg cca tta aat gaa gtt att ggt aca att ttg	1527		
117	Val Ala Val Thr Gly Leu Pro Leu Asn Glu Val Ile Gly Thr Ile Leu			
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120	aag gga aaa tgg gac aat aag aga act gag ttc tct tta cca cca ctg	1575		
121	Lys Gly Lys Trp Asp Asn Lys Arg Thr Glu Phe Ser Leu Pro Pro Leu			
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124	atg aat ctt ttc ctt gga gaa cct gga agt ggt gga tcc tcc aca cca	1623		
125	Met Asn Leu Phe Leu Gly Glu Pro Gly Ser Gly Gly Ser Ser Thr Pro			
126		300	305	310
128	tca atg gta ggt gca gta aag aag tgg caa atg tct gat cca gag aag	1671		
129	Ser Met Val Gly Ala Val Lys Lys Trp Gln Met Ser Asp Pro Glu Lys			
130		315	320	325
132	gca cga gaa aac tgg cag aat ttg tca gat gca aat tta gaa ctg gaa	1719		
133	Ala Arg Glu Asn Trp Gln Asn Leu Ser Asp Ala Asn Leu Glu Leu Glu			
134	330	335	340	345

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140 tat cta cga gtc att aag tct tgt agt gtg ctt act tct gaa aag tgg 1815
141 Tyr Leu Arg Val Ile Lys Ser Cys Ser Val Leu Thr Ser Glu Lys Trp
142          365          370          375
144 gtg tta cat gct act gaa cca atc aac gaa gcc att att aaa gaa ctc 1863
145 Val Leu His Ala Thr Glu Pro Ile Asn Glu Ala Ile Ile Lys Glu Leu
146          380          385          390
148 tta gag gca aga gaa gct atg ttg agg atc aga att ctt atg cgt cag 1911
149 Leu Glu Ala Arg Glu Ala Met Leu Arg Ile Arg Ile Leu Met Arg Gln
150          395          400          405
152 atg ggt gag gcg gct agc gtt ccg ata gag cct gaa tct caa act caa 1959
153 Met Gly Glu Ala Ala Ser Val Pro Ile Glu Pro Glu Ser Gln Thr Gln
154 410          415          420          425
156 ctt ttg gat tct aca atg agt gct gaa gga gtt cta ctt gct ggt gtt 2007
157 Leu Leu Asp Ser Thr Met Ser Ala Glu Gly Val Leu Leu Ala Gly Val
158          430          435          440
160 cct gga gct ggt gga ttt gat gcc ata ttt gca atc act tta ggg gat 2055
161 Pro Gly Ala Gly Gly Phe Asp Ala Ile Phe Ala Ile Thr Leu Gly Asp
162          445          450          455
164 tcc ggc acc aaa ctg acc cag gca tgg agt tcg cac aat gtt ttg gcc 2103
165 Ser Gly Thr Lys Leu Thr Gln Ala Trp Ser Ser His Asn Val Leu Ala
166          460          465          470
168 ttg ttg gtg aga gaa gat cca cat ggc gtt tgc cta gaa agt ggt gat 2151
169 Leu Leu Val Arg Glu Asp Pro His Gly Val Cys Leu Glu Ser Gly Asp
170          475          480          485
172 cca cga acc aca tgt att act tca ggc gtt tca att cac ctt gag 2199
173 Pro Arg Thr Thr Cys Ile Thr Ser Gly Val Ser Ser Ile His Leu Glu
174 490          495          500          505
176 taaacaacat tgttttcagtg tccaattatt aggtgcgtca ccaagttcgg ttgagtatac 2259
178 tgttttgcata atagacttgg gtgctaaaatt tcttggtgta agcattttta taccattgt 2319
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188 <213> ORGANISM: Arabidopsis thaliana
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197 Ala Arg Phe Tyr Ala Ile Val Lys Pro Ile Asn Glu Glu Val Lys Pro
198          35          40          45
200 Glu Ser Trp Ala Trp Lys Trp Thr Asp Val Lys Leu Thr Ser Pro Gln
201          50          55          60
203 Leu Ser Arg Glu Ser Met Tyr Lys Leu Ser Leu Asn His Leu Thr Leu
204 65          70          75          80

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207      85      90      95
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210      100      105      110
212 Glu Ser Leu His Lys Leu Leu Leu Gln Gly Leu Asp Ile Thr Ile Leu
213      115      120      125
215 Gly Ser Asn Asp Phe Tyr Ser Tyr Arg Asn Gln Ile Glu Ser Ala Gly
216      130      135      140
218 Leu Pro Leu Thr Pro Glu Ser Leu Gly Thr Leu Ala Pro Phe Ala Ser
219 145      150      155      160
221 Ile Thr Phe Asn Ala Ala Glu Ser Asn Gly Ala Asn Ser Lys Pro Glu
222      165      170      175
224 Val Ala Lys Thr Gly Leu Gly Ser Ser Ala Ala Met Thr Thr Ala Val
225      180      185      190
227 Val Ala Ala Leu Leu His Tyr Leu Gly Val Val Asp Leu Ser Asp Pro
228      195      200      205
230 Cys Lys Glu Gly Lys Phe Gly Cys Ser Asp Leu Asp Val Ile His Met
231      210      215      220
233 Ile Ala Gln Thr Ser His Cys Leu Ala Gln Gly Lys Val Gly Ser Gly
234 225      230      235      240
236 Phe Asp Val Ser Cys Ala Val Tyr Gly Ser Gln Arg Tyr Val Arg Phe
237      245      250      255
239 Ser Pro Glu Val Leu Ser Phe Ala Gln Val Ala Val Thr Gly Leu Pro
240      260      265      270
242 Leu Asn Glu Val Ile Gly Thr Ile Leu Lys Gly Lys Trp Asp Asn Lys
243      275      280      285
245 Arg Thr Glu Phe Ser Leu Pro Pro Leu Met Asn Leu Phe Leu Gly Glu
246      290      295      300
248 Pro Gly Ser Gly Gly Ser Ser Thr Pro Ser Met Val Gly Ala Val Lys
249 305      310      315      320
251 Lys Trp Gln Met Ser Asp Pro Glu Lys Ala Arg Glu Asn Trp Gln Asn
252      325      330      335
254 Leu Ser Asp Ala Asn Leu Glu Leu Glu Thr Lys Leu Asn Asp Leu Ser
255      340      345      350
257 Lys Leu Ala Lys Asp His Trp Asp Val Tyr Leu Arg Val Ile Lys Ser
258      355      360      365
260 Cys Ser Val Leu Thr Ser Glu Lys Trp Val Leu His Ala Thr Glu Pro
261      370      375      380
263 Ile Asn Glu Ala Ile Ile Lys Glu Leu Leu Glu Ala Arg Glu Ala Met
264 385      390      395      400
266 Leu Arg Ile Arg Ile Leu Met Arg Gln Met Gly Glu Ala Ala Ser Val
267      405      410      415
269 Pro Ile Glu Pro Glu Ser Gln Thr Gln Leu Leu Asp Ser Thr Met Ser
270      420      425      430
272 Ala Glu Gly Val Leu Leu Ala Gly Val Pro Gly Ala Gly Gly Phe Asp
273      435      440      445
275 Ala Ile Phe Ala Ile Thr Leu Gly Asp Ser Gly Thr Lys Leu Thr Gln
276      450      455      460
278 Ala Trp Ser Ser His Asn Val Leu Ala Leu Leu Val Arg Glu Asp Pro

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303 gacatcagaa tcattggcca cccttccgcc ttttgctctc atttctttca atactgatga 540
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314 <222> LOCATION: 715
315 <223> OTHER INFORMATION: n can be any nucleotide
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321 tctcggaaac atttaacact tcagtgtgta tcttcaagtg aatcaaggaa cccttttgta 180
322 gaaaatgcta ttcaatatac tatagcagct gcacatgcaa catttgacaa gaataagaaa 240
323 gaggcattag ataaactact cttacaaggt cttgatatta cgatcttagg ttgcaatgac 300
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335 <211> LENGTH: 571
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VERIFICATION SUMMARY

DATE: 03/25/2002

PATENT APPLICATION: US/09/988,863A

TIME: 09:53:11

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Output Set: N:\CRF3\03252002\I988863A.raw

L:312 M:283 W: Missing Blank Line separator, <220> field identifier
L:330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4